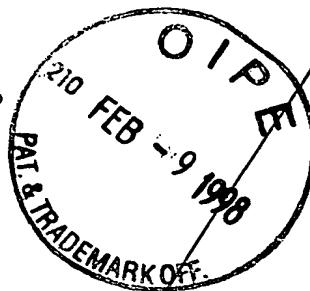


SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: ASHIKARI, Toshihiko  
TANAKA, Yoshikazu  
FUJIWARA, Hiroyuki  
NAKAO, Masahiro  
FUKUI, Yuko  
SAKAKIBARA, Keiko  
MIZUTANI, Masako  
KUSUMI, Takaaki



(ii) TITLE OF INVENTION: GENE ENCODING A PROTEIN HAVING ACYL GROUP TRANSFER ACTIVITY

(iii) NUMBER OF SEQUENCES: 31

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
- (B) STREET: P.O. Box 1404
- (C) CITY: Alexandria
- (D) STATE: Virginia
- (E) COUNTRY: United States
- (F) ZIP: 22313-1404

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/894,356
- (B) FILING DATE: 18-AUG-1997
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: JP 7-67159
- (B) FILING DATE: 17-FEB-1995

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: JP 7-196915
- (B) FILING DATE: 29-JUN-1995

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: JP 8-46534
- (B) FILING DATE: 30-JAN-1996

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: WO PCT/JP96/00348
- (B) FILING DATE: 16-FEB-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Meuth, Donna M.  
(B) REGISTRATION NUMBER: 36,607  
(C) REFERENCE/DOCKET NUMBER: 001560-308

(ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (703) 836-6620  
(B) TELEFAX: (703) 836-2021

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1703 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Gentiana triflora var. japonica  
(F) TISSUE TYPE: petal

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA library  
(B) CLONE: pgAT4

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 6..1412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCATT ATG GAG CAA ATC CAA ATG GTG AAG GTT CTT GAA AAA TGC CAA  
Met Glu Gln Ile Gln Met Val Lys Val Leu Glu Lys Cys Gln  
1 5 10

47

GTT ACA CCA CCA TCT GAC ACA ACA GAT GTC GAG TTA TCG CTA CCG GTA  
Val Thr Pro Pro Ser Asp Thr Thr Asp Val Glu Leu Ser Leu Pro Val  
15 20 25 30

95

ACA TTC TTC GAT ATC CCC TGG TTG CAC TTG AAT AAG ATG CAG TCC CTT  
Thr Phe Phe Asp Ile Pro Trp Leu His Leu Asn Lys Met Gln Ser Leu  
35 40 45

143

CTG TTT TAC GAC TTT CCG TAC CCA AGA ACA CAT TTC TTG GAC ACT GTT  
Leu Phe Tyr Asp Phe Pro Tyr Pro Arg Thr His Phe Leu Asp Thr Val  
50 55 60

191

ATC CCT AAT CTT AAG GCC TCT TTG TCT CTC ACT CTA AAA CAC TAC GTT Ile Pro Asn Leu Lys Ala Ser Leu Ser Leu Thr Leu Lys His Tyr Val 65 70 75	239
CCG CTT AGC GGA AAT TTG TTG ATG CCG ATC AAA TCG GGC GAA ATG CCG Pro Leu Ser Gly Asn Leu Leu Met Pro Ile Lys Ser Gly Glu Met Pro 80 85 90	287
AAG TTT CAG TAC TCC CGT GAT GAG GGC GAC TCG ATA ACT TTG ATC GTT Lys Phe Gln Tyr Ser Arg Asp Glu Gly Asp Ser Ile Thr Leu Ile Val 95 100 105 110	335
GCG GAG TCT GAC CAG GAT TTT GAC TAC CTT AAA GGT CAT CAA CTG GTA Ala Glu Ser Asp Gln Asp Phe Asp Tyr Leu Lys Gly His Gln Leu Val 115 120 125	383
GAT TCC AAT GAT TTG CAT GGC CTT TTT TAT GTT ATG CCA CGG GTT ATA Asp Ser Asn Asp Leu His Gly Leu Phe Tyr Val Met Pro Arg Val Ile 130 135 140	431
AGG ACC ATG CAA GAC TAT AAA GTG ATG CCG CTC GTA GCC GTG CAA GTA Arg Thr Met Gln Asp Tyr Lys Val Ile Pro Leu Val Ala Val Gln Val 145 150 155	479
ACC GTT TTT CCT AAC CGT GGC ATA GGC GTG GCT CTG ACG GCA CAT CAT Thr Val Phe Pro Asn Arg Gly Ile Ala Val Ala Leu Thr Ala His His 160 165 170	527
TCA ATT GCA GAT GCT AAA AGT TTT GTA ATG TTC ATC AAT GCT TGG GCC Ser Ile Ala Asp Ala Lys Ser Phe Val Met Phe Ile Asn Ala Trp Ala 175 180 185 190	575
TAT ATT AAC AAA TTT GGG AAA GAC GCG GAC TTG TTG TCC GCG AAT CTT Tyr Ile Asn Lys Phe Gly Lys Asp Ala Asp Leu Leu Ser Ala Asn Leu 195 200 205	623
CTT CCA TCT TTC GAT AGA TCG ATA ATC AAA GAT CTG TAT GGC CTA GAG Leu Pro Ser Phe Asp Arg Ser Ile Ile Lys Asp Leu Tyr Gly Leu Glu 210 215 220	671
GAA ACA TTT TGG AAC GAA ATG CAA GAT GTT CTT GAA ATG TTC TCT AGA Glu Thr Phe Trp Asn Glu Met Gln Asp Val Leu Glu Met Phe Ser Arg 225 230 235	719
TTT GGA AGC AAA CCC CCT CGA TTC AAC AAG GTA CGA GCT ACA TAT GTC Phe Gly Ser Lys Pro Pro Arg Phe Asn Lys Val Arg Ala Thr Tyr Val 240 245 250	767
CTC TCC CTT GCT GAA ATC CAG AAG CTA AAG AAC AAA GTA CTG AAT CTC Leu Ser Leu Ala Glu Ile Gln Lys Leu Lys Asn Lys Val Leu Asn Leu 255 260 265 270	815
AGA GGA TCC GAA CCG ACA ATA CGT GTA ACG ACG TTC ACA ATG ACG TGT Arg Gly Ser Glu Pro Thr Ile Arg Val Thr Thr Phe Thr Met Thr Cys 275 280 285	863

GGA TAC GTA TGG ACA TGC ATG GTC AAA TCA AAA GAT GAC GTC GTA TCA 911  
Gly Tyr Val Trp Thr Cys Met Val Lys Ser Lys Asp Asp Val Val Ser  
290 295 300

GAG GAA TCA TCG AAC GAC GAA AAT GAG CTC GAG TAC TTC AGT TTT ACA 959  
Glu Glu Ser Ser Asn Asp Glu Asn Glu Leu Glu Tyr Phe Ser Phe Thr  
305 310 315

GCG GAT TGC CGA GGA CTT CTG ACG CCC CCG TGT CCT AAC TAC TTT 1007  
Ala Asp Cys Arg Gly Leu Leu Thr Pro Pro Cys Pro Pro Asn Tyr Phe  
320 325 330

GGC AAC TGT CTT GCG TCA TGC GTT GCA AAA GCA ACA CAT AAA GAG TTA 1055  
Gly Asn Cys Leu Ala Ser Cys Val Ala Lys Ala Thr His Lys Glu Leu  
335 340 345 350

GTT GGG GAT AAA GGG CTT CTT GTT GCA GTT GCA GCT ATT GGA GAA GCC 1103  
Val Gly Asp Lys Gly Leu Leu Val Ala Val Ala Ala Ile Gly Glu Ala  
355 360 365

ATT GAA AAG AGG TTG CAC AAC GAA AAA GGC GTT CTT GCA GAT GCA AAA 1151  
Ile Glu Lys Arg Leu His Asn Glu Lys Gly Val Leu Ala Asp Ala Lys  
370 375 380

ACT TGG TTA TCG GAA TCT AAT GGA ATC CCT TCA AAA AGA TTT CTC GGG 1199  
Thr Trp Leu Ser Glu Ser Asn Gly Ile Pro Ser Lys Arg Phe Leu Gly  
385 390 395

ATT ACC GGA TCG CCT AAG TTC GAT TCG TAT GGT GTA GAT TTT GGA TGG 1247  
Ile Thr Gly Ser Pro Lys Phe Asp Ser Tyr Gly Val Asp Phe Gly Trp  
400 405 410

GGA AAG CCT GCA AAA TTT GAC ATT ACC TCT GTT GAT TAT GCA GAA TTG 1295  
Gly Lys Pro Ala Lys Phe Asp Ile Thr Ser Val Asp Tyr Ala Glu Leu  
415 420 425 430

ATT TAT GTG ATT CAG TCC AGG GAT TTT GAA AAA GGT GTG GAG ATT GGA 1343  
Ile Tyr Val Ile Gln Ser Arg Asp Phe Glu Lys Gly Val Glu Ile Gly  
435 440 445

GTA TCA TTG CCT AAG ATT CAT ATG GAT GCA TTT GCA AAA ATC TTT GAA 1391  
Val Ser Leu Pro Lys Ile His Met Asp Ala Phe Ala Lys Ile Phe Glu  
450 455 460

GAA GGC TTT TGC TGT TTG TCA TAGTCTCTTT AATAGAACCA TATTTGCTGC 1442  
Glu Gly Phe Cys Ser Leu Ser  
465

AATAAAAGTAC CAAGTCCTTT AGTAACACTA CACCAAACCC TACTTCGAG GCAGAACAC 1502

CACAACGAGG TTCAATCACT AGAAGGTTGT ACTTCATAAA TTCCAGAGGT CGAATATACA 1562

CCGTTGTCCT CTGAAAAGTT GAACCTCACCA CCTGACATGG TGTTACGATA GGTATTGTAT 1622

AATGCCATTA TATACTTCCA TAAAGTATCC TATGCAATAG AGAACATGTT ATGTGTTAAA 1682

AAAAAAAAAA AAAAAAAA A

1703

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1622 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Gentiana triflora va. japonica
- (F) TISSUE TYPE: petal

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library
- (B) CLONE: PGAT106

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 35..1471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAACCATTGA ATCCAATTAA TCTGATTAT TAAG ATG GCA GGA AAT TCC GAG Met Ala Gly Asn Ser Glu	52
1 5	
GAT ATC AAA GTT CTT GAG AAA TGC CGT GTT GCG CCA CCA CCG GAC GCC Asp Ile Lys Val Leu Glu Lys Cys Arg Val Ala Pro Pro Pro Asp Ala	100
10 15 20	
GTC GCC GAG TTT ACA GTC CCA CTG TCG TTT TTC GAC ATG CGA TGG TTG Val Ala Glu Phe Thr Val Pro Leu Ser Phe Phe Asp Met Arg Trp Leu	148
25 30 35	
ATC TCT GAT GCA GAA GAC CAT CTG CAT TTC TAC AGA TTC CGC CAT CCT Ile Ser Asp Ala Glu His His Leu His Phe Tyr Arg Phe Arg His Pro	196
40 45 50	
TGT CCC AAC TCT AAA TTT ATC ATT TCA TCC ATT AAA TCG TCC CTT TCC Cys Pro Asn Ser Lys Phe Ile Ile Ser Ser Ile Lys Ser Ser Leu Ser	244
55 60 65 70	
CTT GTT CTC AAA CAC TTT CTT CCG TTA GCC GGG AAT TTG ATT TGG CCG Leu Val Leu Lys His Phe Leu Pro Leu Ala Gly Asn Leu Ile Trp Pro	292
75 80 85	

GTA GAT TCC TCC GAT AGA ATG CCG GAG TTG CGT TAC AAG AAA GGG GAC 340  
Val Asp Ser Ser Asp Arg Met Pro Glu Leu Arg Tyr Lys Lys Gly Asp  
90 95 100

TCC GTT TCT TTA ACA ATT GCA GAA TCG AGC ATG GAT TTT GAT TAT CTC 388  
Ser Val Ser Leu Thr Ile Ala Glu Ser Ser Met Asp Phe Asp Tyr Leu  
105 110 115

GCC GGA GAT CAT CAG AGG GAT TCT TAT AAA TTC AAC GAT TTG ATT CCG 436  
Ala Gly Asp His Gln Arg Asp Ser Tyr Lys Phe Asn Asp Leu Ile Pro  
120 125 130

CAG CTG CCA GAA CCG ATT GTA ACC TCC GGC GAC GAA GTA TTA CCA CTT 484  
Gln Leu Pro Glu Pro Ile Val Thr Ser Gly Asp Glu Val Leu Pro Leu  
135 140 145 150

TTT GCT TTA CAG GTG ACG GTG TTC TCC AAC ACC GGT ATA TGC ATT GGA 532  
Phe Ala Leu Gln Val Thr Val Phe Ser Asn Thr Gly Ile Cys Ile Gly  
155 160 165

CGC AAT CTT CAT CAA GTT CTT GGT GAT GCC AGT TCT TTT CTG CAT TTT 580  
Arg Asn Leu His Gln Val Leu Gly Asp Ala Ser Phe Leu His Phe  
170 175 180

AAT AAA TTA TGG GTT TTG GTT GAC AAA TCC AAT GGA GAT TCA TTA AAG 628  
Asn Lys Leu Trp Val Leu Val Asp Lys Ser Asn Gly Asp Ser Leu Lys  
185 190 195

TTC CTT CCA CTT TCT CTA CCT ATG TAC GAC AGA TCT GTG GTG CAA 676  
Phe Leu Pro Leu Ser Ser Leu Pro Met Tyr Asp Arg Ser Val Val Gln  
200 205 210

GAT CCA TTT CAT ATT CGT CGA AAA ATC TAC AAT GAA AGA AAA CTG CTC 724  
Asp Pro Phe His Ile Arg Arg Lys Ile Tyr Asn Glu Arg Lys Leu Leu  
215 220 225 230

AAA TCT CAG GGC ACA CCT ACT GTT CTA AAT CCA GCA ATT TCT AAA GAT 772  
Lys Ser Gln Gly Thr Pro Thr Val Leu Asn Pro Ala Ile Ser Lys Asp  
235 240 245

GAA GTT CGA GCC ACC TTC ATC CTA CAC CCT ATT GAT ATC ATG AAG CTC 820  
Glu Val Arg Ala Thr Phe Ile Leu His Pro Ile Asp Ile Met Lys Leu  
250 255 260

AAG AAA TTC ATT TCG TCA AAA AAT CGC AAC TTA ACC GGT AGT AGT AAT 868  
Lys Lys Phe Ile Ser Ser Lys Asn Arg Asn Leu Thr Gly Ser Ser Asn  
265 270 275

TAT AAT CTG TCA ACT TTC ACG GTG ACA TCT GCA CTG ATC TGG ACA TGC 916  
Tyr Asn Leu Ser Thr Phe Thr Val Thr Ser Ala Leu Ile Trp Thr Cys  
280 285 290

TTG TCG AAA TCA TTA GAC ACC GTC GTA AGA GAG AAG GTG GAA GAG GAT 964  
Leu Ser Lys Ser Leu Asp Thr Val Val Arg Glu Lys Val Glu Glu Asp  
295 300 305 310

AAA CAT GCA GCA AAC TTA TGT GCT TTC ATC AAC TGC CGA CAA CGT TTT 1012  
Lys His Ala Ala Asn Leu Cys Ala Phe Ile Asn Cys Arg Gln Arg Phe  
315 320 325

GCT CCG CCG ATA CCT CAA AAT TAC TTT GGA AAT TGC ATA GTG CCT TGT 1060  
Ala Pro Pro Ile Pro Gln Asn Tyr Phe Gly Asn Cys Ile Val Pro Cys  
330 335 340

ATG GTG GGA TCG ACT CAT GAG CAA CTT GTA GGA AAT GAA GGG TTG TCG 1108  
Met Val Gly Ser Thr His Glu Gln Leu Val Gly Asn Glu Gly Leu Ser  
345 350 355

GTA GCT GCA ACC GCC ATC GGA GAT GCT ATC CAT AAG AGG TTA CAT GAC 1156  
Val Ala Ala Thr Ala Ile Gly Asp Ala Ile His Lys Arg Leu His Asp  
360 365 370

TAC GAA GGA ATT CTG AGA GGA GAT TGG ATA TCG CCG CCC CGA TCA ACA 1204  
Tyr Glu Gly Ile Leu Arg Gly Asp Trp Ile Ser Pro Pro Arg Ser Thr  
375 380 385 390

TCT GCG GCA CCA AGG TCG ACG CTC ATT TAT GTC GTT GGA TCC GCA CAA 1252  
Ser Ala Ala Pro Arg Ser Thr Leu Ile Tyr Val Val Gly Ser Ala Gln  
395 400 405

CGC AAT GTG CAT GAT TTT GAT GCA GAT TTT GGT TGG GGA AAG CTT GAA 1300  
Arg Asn Val His Asp Phe Asp Ala Asp Phe Gly Trp Gly Lys Leu Glu  
410 415 420

AAG CAT GAA TCT GTT TCA ACT AAT CCT TCG GCA ACA CTA ATT TTG ATC 1348  
Lys His Glu Ser Val Ser Thr Asn Pro Ser Ala Thr Leu Ile Leu Ile  
425 430 435

TCT CGG TCC AGA AGA TTT AAA GGA GCA CTT GAG CTT GGC ATT TCT TTG 1396  
Ser Arg Ser Arg Arg Phe Lys Gly Ala Leu Glu Leu Gly Ile Ser Leu  
440 445 450

CCT AAG AAT AGG ATG GAC GGA TTT GCC ACC ATT TTT ACG AAT TTC ATC 1444  
Pro Lys Asn Arg Met Asp Ala Phe Ala Thr Ile Phe Thr Asn Phe Ile  
455 460 465 470

AAT AGT CTC CAT GTG AGG AGC CCT TTG TAAGAAAAAA GTGGTATCAA 1491  
Asn Ser Leu His Val Arg Ser Pro Leu  
475

TGTATAAAAA AGACAGACAA GTTATGATGC AACAAATGTT TTAGGAGATT ACAAAATCCAT 1551

GGGAAGATGT ATCAAACCTCA TCTCTCTATA TATATATATT CAATTGTTTT AAAAAAAA 1611

AAAAAAAAAA A 1622

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1605 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Petunia hybrida
- (F) TISSUE TYPE: petal

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library
- (B) CLONE: pPAT48

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 67..1410

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGTGACGAA ATCCATTTCA TTTCCTCTTC	TTTCTTGTGTT TTCTAATTTC GTCATCATTG	60
TTATCC ATG GCA GGT GAA GTA GCA AAA GAA GAA GTT ACA AAA GTG AAA	Met Ala Gly Glu Val Ala Lys Gln Glu Val Thr Lys Val Lys	108
1 5 10		
GTC CTG AAA AAA ACA AAC GTG AAA CCA CAT AAA CCA CTA GGA AAA AAA	Val Leu Lys Lys Thr Asn Val Lys Pro His Lys Pro Leu Gly Lys Lys	156
15 20 25 30		
GAG TGT CAA TTG GTA ACA TTT GAT CTT CCT TAC CTA GCT TTC TAT TAC	Glu Cys Gln Leu Val Thr Phe Asp Leu Pro Tyr Leu Ala Phe Tyr Tyr	204
35 40 45		
AAC CAA AAA TTT CTC ATC TAT AAA GGT GCT GAA AAC TTT GAC GAG ACG	Asn Gln Lys Phe Leu Ile Tyr Lys Gly Ala Glu Asn Phe Asp Glu Thr	252
50 55 60		
GTG GAA AAA ATT AAA GAT GGA CTG GCC TTA GTA TTG GTG GAT TTC TAT	Val Glu Lys Ile Lys Asp Gly Leu Ala Leu Val Leu Val Asp Phe Tyr	300
65 70 75		
CAA CTA GCT GGG AAA CTT GGA AAA GAT GAA GAA GGG GTT TTC AGG GTG	Gln Leu Ala Gly Lys Leu Gly Lys Asp Glu Gly Val Phe Arg Val	348
80 85 90		
GAA TAC GAC GAT GAC ATG GAT GGT GTA GAG GTG ACA GTG GCT GTT GCA	Glu Tyr Asp Asp Asp Met Asp Gly Val Glu Val Thr Val Ala Val Ala	396
95 100 105 110		

GAA GAG ATA GAA GTT GCA GAT CTT ACT GAT GAA GAA GGC ACC ACC AAA 444  
Glu Glu Ile Glu Val Ala Asp Leu Thr Asp Glu Glu Gly Thr Thr Lys  
115 120 125

TTG CAG GAC TTG ATT CCT TGT AAT AAA ATC TTG AAT TTG GAA GGG CTT 492  
Leu Gln Asp Leu Ile Pro Cys Asn Lys Ile Leu Asn Leu Glu Gly Leu  
130 135 140

CAT CGC CCT CTT CTA GCT GTG CAG CTC ACC AAG CTC AAG GAC GGG CTC 540  
His Arg Pro Leu Leu Ala Val Gln Leu Thr Lys Leu Lys Asp Gly Leu  
145 150 155

ACC ATG GGA TTA GCA TTT AAC CAT GCT GTG CTG GAT GGT ACT TCG ACG 588  
Thr Met Gly Leu Ala Phe Asn His Ala Val Leu Asp Gly Thr Ser Thr  
160 165 170

TGG CAC TTT ATG ACC TCG TGG TCC GAG CTT TGC TGT GGG TCC ACC TCA 636  
Trp His Phe Met Thr Ser Trp Ser Glu Leu Cys Cys Gly Ser Thr Ser  
175 180 185 190

ATT TCT GTC CCA CCA TTC CTT GAA CGA ACC AAG GGT CGT AAC ACT CGA 684  
Ile Ser Val Pro Pro Phe Leu Glu Arg Thr Lys Ala Arg Asn Thr Arg  
195 200 205

GTC AAG CTC AAC CTC TCT CAA CCA TCA GAT GCA CCC GAA CAT GCT AAG 732  
Val Lys Leu Asn Leu Ser Gln Pro Ser Asp Ala Pro Glu His Ala Lys  
210 215 220

TCA GCA ACC AAC GGT GAT GTC CCG GCC AAC GTA GAC CCA CCT CTT CGC 780  
Ser Ala Thr Asn Gly Asp Val Pro Ala Asn Val Asp Pro Pro Leu Arg  
225 230 235

GAA AGA GTA TTC AAG TTC TCC GAG TTA GCA ATT GAC AAA ATC AAG TCA 828  
Glu Arg Val Phe Lys Phe Ser Glu Leu Ala Ile Asp Lys Ile Lys Ser  
240 245 250

ACA GTC AAT GCC AAC TCA GGA GAG ACG CCA TTC TCC ACA TTC CAA TCA 876  
Thr Val Asn Ala Asn Ser Gly Glu Thr Pro Phe Ser Thr Phe Gln Ser  
255 260 265 270

CTC TCC GCA CAC GTG TGG CTA GCC GTC ACA CGT GCG CGC CAA CTC AAG 924  
Leu Ser Ala His Val Trp Leu Ala Val Thr Arg Ala Arg Gln Leu Lys  
275 280 285

CCC GAG GAC TAC ACT GTG TAC ACT GTG TTT GCT GAT TGC AGG AAA AGG 972  
Pro Glu Asp Tyr Thr Val Tyr Thr Val Phe Ala Asp Cys Arg Lys Arg  
290 295 300

GTT GAT CCT CCA ATG CCA GAA AGT TAC TTC GGC AAC CTA ATT CAG GCA 1020  
Val Asp Pro Pro Met Pro Glu Ser Tyr Phe Gly Asn Leu Ile Gln Ala  
305 310 315

ATT TTC ACA GTG ACC GCG GCA GGT TTG TTA CTA GCA AGC CCG ATC GAG 1068  
Ile Phe Thr Val Thr Ala Ala Gly Leu Leu Leu Ala Ser Pro Ile Glu  
320 325 330

TTC GCT GGT GGG ATG ATA CAA CAA GCG ATC GTG AAG CAT GAC GCT AAG 1116  
Phe Ala Gly Gly Met Ile Gln Gln Ala Ile Val Lys His Asp Ala Lys  
335 340 345 350

GCC ATT GAT GAA AGA AAC AAG GAG TGG GAG AGC AAC CCG AAG ATC TTT 1164  
Ala Ile Asp Glu Arg Asn Lys Glu Trp Glu Ser Asn Pro Lys Ile Phe  
355 360 365

CAG TAC AAA GAT GCT GGA GTG AAC TGT GTT GCT GTT GGA AGT TCG CCA 1212  
Gln Tyr Lys Asp Ala Gly Val Asn Cys Val Ala Val Gly Ser Ser Pro  
370 375 380

AGG TTC AAG GTT TAC GAC GTG GAT TTT GGA TGG GGA AAG CCA GAG AGT 1260  
Arg Phe Lys Val Tyr Asp Val Asp Phe Gly Trp Gly Lys Pro Glu Ser  
385 390 395

GTG AGG AGT GGT TCG AAC AAT AGG TTT GAT GGA ATG GTG TAT TTG TAC 1308  
Val Arg Ser Gly Ser Asn Asn Arg Phe Asp Gly Met Val Tyr Leu Tyr  
400 405 410

CAA GGC AAA AAT GGA GGA AGA AGC ATT GAT GTG GAG ATT AGT TTG GAA 1356  
Gln Gly Lys Asn Gly Gly Arg Ser Ile Asp Val Glu Ile Ser Leu Glu  
415 420 425 430

GCA AAT GCT ATG GAG AGG TTG GAG AAA GAT AAA GAG TTC CTC ATG GAA 1404  
Ala Asn Ala Met Glu Arg Leu Glu Lys Asp Lys Glu Phe Leu Met Glu  
435 440 445

ACT GCT TAATTTGCTT AGCTTGGACT CAACTGGCTA CACTTTATTT ATGAGCTGCT 1460  
Thr Ala

ATGACTCACAC TGCATGTATG TTTATTATTT TTGGAGGGGT TCTTCCCTTT TATTGTTTC 1520

TATGTTTTT CTTTCTTGTA CGTTATGAAG AGAAACCGAG TATAAAGGAA TAATGTTTC 1580

AGTTATTAAA AAAAAAAA AAAAA 1605

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Perilla ocimoides*

(F) TISSUE TYPE: leaf

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library  
(B) CLONE: pSAT208

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 3..1340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CC GTG ATC GAA ACG TGT AGA GTT GGG CCG CCG CCG GAC TCG GTG GCG	47
Val Ile Glu Thr Cys Arg Val Gly Pro Pro Pro Asp Ser Val Ala	
1 5 10 15	
GAG CAA TCG GTG CCG CTC ACA TTC TTC GAC ATG ACG TGG CTG CAT TTT	95
Glu Gln Ser Val Pro Leu Thr Phe Phe Asp Met Thr Trp Leu His Phe	
20 25 30	
CAT CCC ATG CTT CAG CTC CTC TTC TAC GAA TTC CCT TGT TCC AAG CAA	143
His Pro Met Leu Gln Leu Leu Phe Tyr Glu Phe Pro Cys Ser Lys Gln	
35 40 45	
CAT TTT TCA GAA TCC ATC GTT CCA AAA CTC AAA CAA TCT CTC TCT AAA	191
His Phe Ser Glu Ser Ile Val Pro Lys Leu Lys Gln Ser Leu Ser Lys	
50 55 60	
ACT CTC ATA CAC TTC TTC CCT CTC TCA TGC AAT TTA ATC TAC CCT TCA	239
Thr Leu Ile His Phe Phe Pro Leu Ser Cys Asn Leu Ile Tyr Pro Ser	
65 70 75	
TCC CCG GAG AAA ATG CCG GAG TTT CGG TAT CTA TCC GGG GAC TCG GTT	287
Ser Pro Glu Lys Met Pro Glu Phe Arg Tyr Leu Ser Gly Asp Ser Val	
80 85 90 95	
TCT TTC ACC ATC GCA GAA TCT AGC GAC GAC TTC GAT GAT CTC GTC GGA	335
Ser Phe Thr Ile Ala Glu Ser Ser Asp Asp Phe Asp Asp Leu Val Gly	
100 105 110	
AAT CGT CCA GAA TCT CCC GTT AGG CTC TAC AAC TTT GTC CCT AAA TTG	383
Asn Arg Pro Glu Ser Pro Val Arg Leu Tyr Asn Phe Val Pro Lys Leu	
115 120 125	
CCG CCC ATT GTC GAA GAA TCC GAT AGA AAA CTC TTC CAA GTT TTC GCC	431
Pro Pro Ile Val Glu Glu Ser Asp Arg Lys Leu Phe Gln Val Phe Ala	
130 135 140	
GTG CAG GTG ACT CTT TTC CCA GGC CGA GGC GTC GGT ATT GGA ATA GCA	479
Val Gln Val Thr Leu Phe Pro Gly Arg Gly Val Gly Ile Gly Ile Ala	
145 150 155	
ACG CAT CAC ACC GTT AGC GAC GCC CCG TCG TTT CTC GCG TTT ATA ACG	527
Thr His His Thr Val Ser Asp Ala Pro Ser Phe Leu Ala Phe Ile Thr	

160                    165                    170                    175                    575  
GCT TGG TCT TCA ATG AGC AAA CAC ATT GAA AAT GAA GAT GAA GAT GAA  
Ala Trp Ser Ser Met Ser Lys His Ile Glu Asn Glu Asp Glu Asp Glu  
180                    185                    190                    190  
GAA TTT AAA TCT TTG CCA GTT TTC GAT AGA TCC GTC ATA AAA TAT CCG                    623  
Glu Phe Lys Ser Leu Pro Val Phe Asp Arg Ser Val Ile Lys Tyr Pro  
195                    200                    205  
ACG AAA TTT GAC TCC ATT TAT TGG AGA AAC GCG CTA AAA TTT CCT TTG                    671  
Thr Lys Phe Asp Ser Ile Tyr Trp Arg Asn Ala Leu Lys Phe Pro Leu  
210                    215                    220  
CAA TCT CGT CAT CCC TCA TTA CCG ACG GAC CGC ATT CGA ACC ACG TTC                    719  
Gln Ser Arg His Pro Ser Leu Pro Thr Asp Arg Ile Arg Thr Thr Phe  
225                    230                    235  
GTT TTC ACC CAA TCC AAA ATT AAG AAA TTG AAG GGT TGG ATT CAG TCC                    767  
Val Phe Thr Gln Ser Lys Ile Lys Lys Leu Lys Gly Trp Ile Gln Ser  
240                    245                    250                    255  
AGA GTT CCA AGT TTA GTC CAT CTC TCA TCT TTT GTA GCG ATT GCA GCT                    815  
Arg Val Pro Ser Leu Val His Leu Ser Ser Phe Val Ala Ile Ala Ala  
260                    265                    270  
TAT ATG TGG GCT GGC ATA ACG AAA TCA TTC ACA GCA GAT GAA GAC CAA                    863  
Tyr Met Trp Ala Gly Ile Thr Lys Ser Phe Thr Ala Asp Glu Asp Gln  
275                    280                    285  
GAC AAC GAG GAT GCA TTT TTC TTG ATT CCG GTC GAT CTA AGG CCA CGA                    911  
Asp Asn Glu Asp Ala Phe Phe Leu Ile Pro Val Asp Leu Arg Pro Arg  
290                    295                    300  
TTA GAT CCG CCG GTT CCT GAA AAT TAC TTC GGG AAC TGC TTA TCG TAC                    959  
Leu Asp Pro Pro Val Pro Glu Asn Tyr Phe Gly Asn Cys Leu Ser Tyr  
305                    310                    315  
GCG CTG CCG AGA ATG CGG CGG CGA GAG CTG GTG GGA GAG AAA GGG GTG                    1007  
Ala Leu Pro Arg Met Arg Arg Glu Leu Val Gly Glu Lys Gly Val  
320                    325                    330                    335  
TTT CTG GCA GCT GAG GTA ATC GCG GCG GAG ATA AAA AAA AGG ATC AAC                    1055  
Phe Leu Ala Ala Glu Val Ile Ala Ala Glu Ile Lys Lys Arg Ile Asn  
340                    345                    350  
GAC AAG AGA ATA TTA GAA ACG GTG GAG AAA TGG TCG CCG GAG ATT CGT                    1103  
Asp Lys Arg Ile Leu Glu Thr Val Glu Lys Trp Ser Pro Glu Ile Arg  
355                    360                    365  
AAA GCG TTG CAG AAA TCA TAT TTT TCG GTG GCA GGA TCG AGC AAG CTA                    1151  
Lys Ala Leu Gln Lys Ser Tyr Phe Ser Val Ala Gly Ser Ser Lys Leu  
370                    375                    380

GAT CTT TAC GGT GCA GAT TTT GGA TGG GGG AAG GCG AGA AAG CAA GAA Asp Leu Tyr Gly Ala Asp Phe Gly Trp Gly Lys Ala Arg Lys Gln Glu 385 390 395	1199
ATA TTG TCG ATT GAT GGG GAG AAA TAT GCA ATG ACG CTT TGT AAA GCC Ile Leu Ser Ile Asp Gly Glu Lys Tyr Ala Met Thr Leu Cys Lys Ala 400 405 410 415	1247
AGG GAT TTC GAA GGA GGA TTG GAG GTT TGC TTG TCT TTG CCT AAG GAC Arg Asp Phe Glu Gly Leu Glu Val Cys Leu Ser Leu Pro Lys Asp 420 425 430	1295
AAA ATG GAT GCT TTT GCT GCT TAT TTT TCA CTG GGA ATT AAT GGT Lys Met Asp Ala Phe Ala Ala Tyr Phe Ser Leu Gly Ile Asn Gly 435 440 445	1340
TAATAAATGT ATGTAATTAA ACTAATATTA TTATGTAACA ATTAATTAAG TGTTGAGTAA	1400
CGTGAAGAAT AATCCCTATT ATATATTAT GATTTGGTTC AAATAAAGTG TAAAGCCTCT	1460
TGAAAAAAA AAAAAAAA	1479

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1508 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Senecio cruentus*
  - (F) TISSUE TYPE: petal
- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: cDNA library
  - (B) CLONE: pCAT8
- (ix) FEATURE:
- (A) NAME/KEY: CDS
  - (B) LOCATION: 3..1364
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TG AAC ATT CTC GAA CAT GCC CGA ATA TCG GCC CCC TCG GGC ACC ATC Asn Ile Leu Glu His Ala Arg Ile Ser Ala Pro Ser Gly Thr Ile 1 5 10 15	47
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GGC CAT CGC TCG TTA TCT CTT ACT TTC TTC GAC ATT ACT TGG CTA CTC 95  
Gly His Arg Ser Leu Ser Leu Thr Phe Phe Asp Ile Thr Trp Leu Leu  
20 25 30

TTC CCT CCG GTC CAC CAT CTT TTC TAT GAC TTT CCA CAT TCT AAA 143  
Phe Pro Pro Val His His Leu Phe Phe Tyr Asp Phe Pro His Ser Lys  
35 40 45

TCC CAT TTC ATG GAC ACT ATT GTT CCC AGG CTA AAA CAA TCT TTA TCG 191  
Ser His Phe Met Asp Thr Ile Val Pro Arg Leu Lys Gln Ser Leu Ser  
50 55 60

GTC ACT CTT CAA CAT TTT TTC CCG TTT GCT AGT AAT TTG ATT GTA TTT 239  
Val Thr Leu Gln His Phe Phe Pro Phe Ala Ser Asn Leu Ile Val Phe  
65 70 75

CCT AAC ACT GAT GGT TCG GGT TTT AAT AAA AAA CCA GAA ATA AAA CAC 287  
Pro Asn Thr Asp Gly Ser Gly Phe Asn Lys Lys Pro Glu Ile Lys His  
80 85 90 95

GTT GAA GGT GAT TCT GTT GTG GTT ACT TTT GCA GAA TGT TGT CTT GAC 335  
Val Glu Gly Asp Ser Val Val Val Thr Phe Ala Glu Cys Cys Leu Asp  
100 105 110

TTT AAT AAT TTG ACA GGA AAT CAT CCT GGA AAA TGT GAA AAC TTT TAT 383  
Phe Asn Asn Leu Thr Gly Asn His Pro Arg Lys Cys Glu Asn Phe Tyr  
115 120 125

CCA CTT GTA CCT TCA TTG GGA AAT GCA ATC AAA TTA TGT GAT TGC GTC 431  
Pro Leu Val Pro Ser Leu Gly Asn Ala Ile Lys Leu Cys Asp Cys Val  
130 135 140

ACG GTC CCA CTT TTT TCA CTT CAA GTG ACG TTT TTT CCG GGC TCG GGT 479  
Thr Val Pro Leu Phe Ser Leu Gln Val Thr Phe Phe Pro Gly Ser Gly  
145 150 155

ATA TCA CTA GGA ATG ACG AAT CAT CAT AGC CTT GGT GAC GCT AGC ACG 527  
Ile Ser Leu Gly Met Thr Asn His His Ser Leu Gly Asp Ala Ser Thr  
160 165 170 175

CGG TTC AAC TTT TTG AAA GGG TGG ACT TCG ATT ATT CAA TCT GGT GTA 575  
Arg Phe Asn Phe Leu Lys Gly Trp Thr Ser Ile Ile Gln Ser Gly Val  
180 185 190

GAT CGG TCT TTT TTA ACG AAA GGA TCT CCA CCG GTT TTT GAT AGA TTG 623  
Asp Arg Ser Phe Leu Thr Lys Gly Ser Pro Pro Val Phe Asp Arg Leu  
195 200 205

ATT AAC ATC CCA CAT TTA GAT GAA AAT AAG TTG AGA CAT ACA AGG CTC 671  
Ile Asn Ile Pro His Leu Asp Glu Asn Lys Leu Arg His Thr Arg Leu  
210 215 220

GAA AGT TTT TAT AAA CCT TCG AGC CTT GTT GGT CCC ACT GAT AAA GTT 719  
Glu Ser Phe Tyr Lys Pro Ser Ser Leu Val Gly Pro Thr Asp Lys Val  
225 230 235

CGG TCA ACG TTT GTG TTG ACC CGA ACT AAT ATC AAT CTA CTA AAG AAA 767  
Arg Ser Thr Phe Val Leu Thr Arg Thr Asn Ile Asn Leu Leu Lys Lys  
240 245 250 255

AAG GTC TTA ACC CAA GTG CCA AAC TTG GAG TAC ATG TCA TCT TTT ACG 815  
Lys Val Leu Thr Gln Val Pro Asn Leu Glu Tyr Met Ser Ser Phe Thr  
260 265 270

GTA ACT TGT GGT TAT ATA TGG AGT TGC ATA GCG AAA TCA CTC GTA AAA 863  
Val Thr Cys Gly Tyr Ile Trp Ser Cys Ile Ala Lys Ser Leu Val Lys  
275 280 285

ATA GGA GAA AGA AAG GGC GAA GAC GAG TTA GAA CAG TTC ATA ATC ACC 911  
Ile Gly Glu Arg Lys Gly Glu Asp Glu Leu Glu Gln Phe Ile Ile Thr  
290 295 300

ATT GAT TGT CGA TCT CGT CTT GAT CCA CCA ATT CCC ACA GCC TAC TTT 959  
Ile Asp Cys Arg Ser Arg Leu Asp Pro Pro Ile Pro Thr Ala Tyr Phe  
305 310 315

GGT AAC TGT GGT GCA CCA TGT GTC CCG ACC TTA AAA AAT GTC GTT TTG 1007  
Gly Asn Cys Gly Ala Pro Cys Val Pro Thr Leu Lys Asn Val Val Leu  
320 325 330 335

ACT ACG GAA AAT GGG TAT GCA CTT GGT GCT AAA GTA ATT GGA GAG TCT 1055  
Thr Thr Glu Asn Gly Tyr Ala Leu Gly Ala Lys Val Ile Gly Glu Ser  
340 345 350

ATA TGC AAA ATG ATA TAT AAT AAG GAC GGA ATC TTG AAA GAT GCC GCG 1103  
Ile Cys Lys Met Ile Tyr Asn Lys Asp Gly Ile Leu Lys Asp Ala Ala  
355 360 365

AGA TGG CAT GAA CCT TTC ATG ATC CCG GCT AGG AAG ATT GGT GTT GCT 1151  
Arg Trp His Glu Pro Phe Met Ile Pro Ala Arg Lys Ile Gly Val Ala  
370 375 380

GGT ACA CCT AAG CTC AAC TTG TAC GAC TTT GAT TTT GGG TGG GGG AAG 1199  
Gly Thr Pro Lys Leu Asn Leu Tyr Asp Phe Asp Phe Gly Trp Gly Lys  
385 390 395

CGC ATA AAG TAT GAG ACT GTT TCA ATA GAC TAT AAT ACG TCG ATT TCT 1247  
Arg Ile Lys Tyr Glu Thr Val Ser Ile Asp Tyr Asn Thr Ser Ile Ser  
400 405 410 415

ATA AAT GCA AGC AAA ACA TCA GCA CAA GAT CTT GAA ATT GGA TTG AGT 1295  
Ile Asn Ala Ser Lys Thr Ser Ala Gln Asp Leu Glu Ile Gly Leu Ser  
420 425 430

CTA CCG AGT ATG CAA ATG GAG GCG TTT TCT AGC ATC TTT GAT GAA GGA 1343  
Leu Pro Ser Met Gln Met Glu Ala Phe Ser Ser Ile Phe Asp Glu Gly  
435 440 445

TTA GAG AGT CAA GTT TCA TTG TAGATCATCG TCCCCTTTTT GTGTGCATCA 1394  
Leu Glu Ser Gln Val Ser Leu  
450

AGTTTCTGTC GTTTTATGA GTTGCCACTG TTCTATTCTT TAAGTATAACC TTTCCACTAT 1454  
GTTTTGAAGA TGCAACGATA TAAAATGAAA AAAAAAAA AAAAAAAA AAAA 1508

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lavandula angustifolia
- (F) TISSUE TYPE: petal

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA library
- (B) CLONE: PLAT21

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..1352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

-TG ACC ACC CTC CTC GAA TCG TCC CGA GTG GCG CCG CCT CCA GGC ACG 47  
Xxx Thr Thr Leu Leu Glu Ser Ser Arg Val Ala Pro Pro Pro Gly Thr  
1 5 10 15

GTG GCT GAG CAG TCA CTC CCG CTC ACC TTC TTC GAC ATG ACG TGG CTG 95  
Val Ala Glu Gln Ser Leu Pro Leu Thr Phe Phe Asp Met Thr Trp Leu  
20 25 30

CAT TTC CAC CCC ATG CTT CAG CTT CTC TTC TAC GAA CTC CCC TGT TCC 143  
His Phe His Pro Met Leu Gln Leu Leu Phe Tyr Glu Leu Pro Cys Ser  
35 40 45

AAA CCC GCC TTC CTC GAA ACC GTC GTT CCG AAA CTC AAA CAA TCC TTA 191  
Lys Pro Ala Phe Leu Glu Thr Val Val Pro Lys Leu Lys Gln Ser Leu  
50 55 60

TCT CTA ACC CTC AAA CAC TTC CCC CTT TCA TGC AAT CTA ATC TAC 239  
Ser Leu Thr Leu Lys His Phe Phe Pro Leu Ser Cys Asn Leu Ile Tyr  
65 70 75

CCT CTA TCG CCG GAG AAA ATG CCG GAG TTC CGG TAT CAG AAC GGT GAC Pro Leu Ser Pro Glu Lys Met Pro Glu Phe Arg Tyr Gln Asn Gly Asp 80 85 90 95	287
TCG GTT TCT TTC ACG ATT ATG GAG TCT GTC GGA GAT CAT CCG GAT TCC Ser Val Ser Phe Thr Ile Met Glu Ser Val Gly Asp His Pro His Ser 100 105 110	335
GCT CAT AAA TAC TAC TGC TTT GCC CCT AGC GAC GAT TAT GAA GAT CTC Ala His Lys Tyr Tyr Cys Phe Ala Pro Ser Asp Asp Tyr Glu Asp Leu 115 120 125	383
CAG CTG CCG CCG ATA GTC GAG GAA TCT GAT CGG AAA TTG TTT CAA GTT Gln Leu Pro Pro Ile Val Glu Ser Asp Arg Lys Leu Phe Gln Val 130 135 140	431
TTA GCC GTG CAA GTG ACT CTG TTT CCC GGT CGC GGG GTG TGC ATC GGA Leu Ala Val Gln Val Thr Leu Phe Pro Gly Arg Gly Val Cys Ile Gly 145 150 155	479
ATA ACG ACG CAC CAC ACC GTT AGC GAT GCT CCA TCG TTT GTA GGG TTT Ile Thr Thr His His Thr Val Ser Asp Ala Pro Ser Phe Val Gly Phe 160 165 170 175	527
ATG AAG AGT TGG GCT TCC ATC ACT AAA TTC GGA GGA GAT GAT GAA TTC Met Lys Ser Trp Ala Ser Ile Thr Lys Phe Gly Gly Asp Asp Glu Phe 180 185 190	575
TTG GAC GGA AAA GGT GAA TGT TTG CCG GTT TTC GAC CGA TCG CTC GTG Leu Asp Gly Lys Gly Glu Cys Leu Pro Val Phe Asp Arg Ser Leu Val 195 200 205	623
AAT TAT CCG CCT AAA TTG GAC ACA TAT TTA TGG AAC AAC GCG CAG AAA Asn Tyr Pro Pro Lys Leu Asp Thr Tyr Leu Trp Asn Asn Ala Gln Lys 210 215 220	671
CGT CCG TTG GAA TCG CAG CAT CCA TCT TTA CCG ACG GAT CGG ATT CGA Arg Pro Leu Glu Ser Gln His Pro Ser Leu Pro Thr Asp Arg Ile Arg 225 230 235	719
GCT ACC TAC CTT TTC ACC CAA TCT GAA ATT AAG AAA TTG AAG GGT TTG Ala Thr Tyr Leu Phe Thr Gln Ser Glu Ile Lys Lys Leu Lys Gly Leu 240 245 250 255	767
ATT CAG AGA AAA GCC CCA AAT GTA GTT AAT CTC TCT TCC TTC GTC GCG Ile Gln Arg Lys Ala Pro Asn Val Val Asn Leu Ser Ser Phe Val Ala 260 265 270	815
ATC GCA GCT TAT ATC TGG ACC GGC ATC GCC AAA TCG GTC GGA GAT TAC Ile Ala Ala Tyr Ile Trp Thr Gly Ile Ala Lys Ser Val Gly Asp Tyr 275 280 285	863
AAA GAC GTG GAT GAC GAC AAA CGC GCT TTC TTT TTA ATT CCG ATC GAT Lys Asp Val Asp Asp Asp Lys Arg Ala Phe Phe Leu Ile Pro Ile Asp 290 295 300	911

TTA AGG CCG CGT TTG GAT CCG CCG GCT CCG GGG AAC TAC TTC GGA AAC Leu Arg Pro Arg Leu Asp Pro Pro Ala Pro Gly Asn Tyr Phe Gly Asn 305 310 315	959
TGT CTA TCG TTT GCG ATG GCG AAG ATC CTG CGG CGG GAT TTG GTC GGA Cys Leu Ser Phe Ala Met Ala Lys Ile Leu Arg Arg Asp Leu Val Gly 320 325 330 335	1007
GAT GAA GGG GTG TTT CGG GCA GCT GAG GCG ATC GCG GCG GAA ATA GAG Asp Glu Gly Val Phe Arg Ala Ala Glu Ala Ile Ala Ala Glu Ile Glu 340 345 350	1055
AAG AGG ACG AGC GAC AAG AAG ATT CTA GAA ACT GTG GAG AAC TGG CCG Lys Arg Thr Ser Asp Lys Lys Ile Leu Glu Thr Val Glu Asn Trp Pro 355 360 365	1103
TCT GAG ATT CGC GAA GCC TTG CAA AAC TGT TAT TTC TCG GTG GCG GGA Ser Glu Ile Arg Glu Ala Leu Gln Asn Cys Tyr Phe Ser Val Ala Gly 370 375 380	1151
TCG AGC AGG CTT GAT CTT TAC GGC GCG GAT TTT GGA TGG GGT AAG GCG Ser Ser Arg Leu Asp Leu Tyr Gly Ala Asp Phe Gly Trp Gly Lys Ala 385 390 395	1199
GTG AAG CAA GAG ATA CTG TCG ATT GAT GGA GAG AAG TTT ACG ATG TCG Val Lys Gln Glu Ile Leu Ser Ile Asp Gly Glu Lys Phe Thr Met Ser 400 405 410 415	1247
TTG TGT AAA CCG AGG GAT GCT GCC GGA GGA TTG GAG GTT GGA TTG TCT Leu Cys Lys Pro Arg Asp Ala Ala Gly Gly Leu Glu Val Gly Leu Ser 420 425 430	1295
TTG CCA AAG GAG GAA TTG CAA GCT TTT GAT GAT TAT TTT GCG GAG GGA Leu Pro Lys Glu Glu Leu Gln Ala Phe Asp Asp Tyr Phe Ala Glu Gly 435 440 445	1343
ATA AAG GGT TGATTAATCA TTTAATGATG TATTATGAAG TTGGATGAAA Ile Lys Gly 450	1392
TCCTCTGTTT CATCTCTATT GTTTAACCAA TAATTTTTT CCATTGAAC TTTTGAGTC AATAAAAAAA AAAAAAAA AAAAAAATG AAAAAACTCA GTTATTTTTT TTTTTTTTTT TTTTTTTTT	1452 1512 1521

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Arg Phe Leu Gly Ile Thr Gly Ser Pro Lys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ile His Met Asp Ala Phe Ala Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Gly Val Glu Ile Gly Val Ser Leu Pro Lys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ala Ser Leu Ser Leu Thr Leu Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

His Tyr Val Pro Leu Ser Gly Asn Leu Leu Met Pro Ile Lys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Val Arg Ala Thr Tyr Val Leu Ser Leu Ala Glu Ile Gln Lys  
1 5 10

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ile His Met Asp Ala Phe Ala Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Lys Ile His Met Asp Ala Phe Ala Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Lys Ile His Met Asp Ala Phe Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AARATHCAYA TGGAYGCNTT YGC

23

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CTCGAGTTTT TTTTTTTTTT TTT

23

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTCACCATGG AGCAAATCCA AATGGT

26

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CGAGTCGCC CGTCATCAC

17

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AACAGCTATG ACCATG

16

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Asp Phe Gly Trp Gly Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GAYTTYGGNT GGGGNAA

17

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TGGCAACTGT CTTGCGTCAT G

21

(2) INFORMATION FOR SEQ ID NO:24:

- B
- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 23 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCATGTCAGG TGTGAGGTTC AAC

23

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATCGTTTGC ATGATTGAAC

20

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TCAGAAGAAC TCGTCAAGAA

20

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 12..53

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GGGATCCAAC A ATG GAG CAA ATC CAA ATG GTG GCC GTG ATC GAA ACG TGT  
Met Glu Gln Ile Gln Met Val Ala Val Ile Glu Thr Cys  
1 5 10

50

AGA  
Arg

53

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTAAAACGAC GGCCAT

16

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 12..45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGGATCCAAC A ATG GAG CAA ATC CAA ATG GTG AAC ATT CTC GAA C  
Met Glu Gln Ile Gln Met Val Asn Ile Leu Glu  
15 20 25

45

(2) INFORMATION FOR SEQ ID NO:30:

- B'
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CTCGGAGGAA TTCGGCACGA C

21

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 18..35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AGTCGGATCC AACAAATG ACC ACC CTC CTC GAA TCC  
Thr Thr Leu Leu Glu Ser  
15

35

B' conclusio